

SEQUENCE LISTING

<110> Xia, Zhi-Qiang
Costa, Michael A
Davin, Laurence B
Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
Methods of Use

<130> WSUR116430

<140> 09/673,918

<141> 2000-10-23

<150> PCT/US99/08975

<151> 1999-04-23

<150> 60/082,977

<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 819

<212> DNA

<213> Forsythia x intermedia

<220>

<221> CDS

<222> (1)..(819)

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Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu	
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ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	

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Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala				
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gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca				336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala				
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gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc				384
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys				
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atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata				432
Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile				
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att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat				480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His				
	145	150	155	160
gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg				528
Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu				
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gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct				576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro				
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Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn				
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Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly				
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Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala				
	225	230	235	240
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga				768
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly				
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ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat				816
Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp				
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tct				819
Ser				

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 <213> Forsythia x intermedia

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Ala	Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Ala	Leu	Thr	Arg	Asn	Leu
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Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn	Cys	Leu	Ser	Pro
			180					185					190		
Phe	Gly	Leu	Pro	Thr	Ala	Leu	Gly	Lys	Lys	Phe	Ser	Gly	Ile	Lys	Asn
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Glu	Glu	Glu	Phe	Glu	Asn	Val	Ile	Asn	Phe	Ala	Gly	Asn	Leu	Lys	Gly
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Pro	Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala	Leu	Tyr	Leu	Ala
225					230					235					240
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Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp
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Ser

<210> 3

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<212> DNA

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<220>

<221> CDS

<222> (1)..(831)

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gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa acc	96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr	
20 25 30	
aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat	144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp	
35 40 45	
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc	192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser	
50 55 60	
aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa	240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys	
65 70 75 80	
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg	288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	
85 90 95	
ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac	336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp	
100 105 110	
aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga	384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly	
115 120 125	
gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc	432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg	

130	135	140	
agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt			480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly			
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ggg tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt			528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu			
	165	170	175
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat			576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn			
	180	185	190
tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca			624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser			
	195	200	205
ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga			672
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly			
	210	215	220
aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct			720
Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala			
	225	230	235
ctt tat ctg gct agt gat gag gca aaa tac gtg agt gga cac aat ctg			768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
	245	250	255
ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc			816
Phe Ile Asp Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe			
	260	265	270
caa tat cca gat tct			831
Gln Tyr Pro Asp Ser			
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 35 40 45

Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
50 55 60

Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
65 70 75 80

Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
85 90 95

Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
100 105 110

Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
115 120 125

Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
130 135 140

Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
145 150 155 160

Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
165 170 175

Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
180 185 190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
195 200 205

Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
210 215 220

Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
225 230 235 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
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Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
260 265 270

Gln Tyr Pro Asp Ser
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<210> 5

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<221> CDS

<222> (1)..(819)

<220>

<221> misc_feature

<222> (1)..(819)

<223> cDNA molecule encoding secoisolariciresinol dehydrogenase wherein
Xaa = any amino acid

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Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala	
1 5 10 15	
ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc	96
Leu Ile Thr Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu	
20 25 30	
ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	
65 70 75 80	
aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca	288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala	
85 90 95	
gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca	336
Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala	
100 105 110	
gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt	384
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe	
115 120 125	
atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata	432
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile	
130 135 140	
att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat	480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His	
145 150 155 160	
gct tat tgt ggt gca aaa cat gct gta tta ggc ctt act agg aat ctg	528
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu	
165 170 175	

gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct 576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
180 185 190

ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat 624
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
195 200 205

gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt 672
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
210 215 220

aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct 720
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
225 230 235 240

agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga 768
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
245 250 255

ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac 816
Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
260 265 270

tct 819
Ser

<210> 6

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<213> Forsythia x intermedia

<220>

<221> misc_feature

<222> (1)..(273)

<223> Secoisolariciresinol dehydrogenase wherein Xaa = any amino acid

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Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
20 25 30

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
35 40 45

Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
50 55 60

Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp

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Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala						
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Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala						
	100		105			110
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe						
	115		120			125
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile						
	130		135		140	
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His						
145		150		155		160
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu						
	165		170			175
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro						
	180		185			190
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn						
	195		200		205	
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly						
	210		215		220	
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala						
225		230		235		240
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly						
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Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp						
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Ser

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Gly	Lys	Val	Ala	Leu	Ile	Thr	Gly	Gly	Ala	Ser	Gly	Ile	Gly	Glu	Phe	
			20					25					30			
aca	gca	aaa	ctc	ttc	tcc	caa	cat	gga	gcc	aaa	gtt	gcc	att	gct	gat	144
Thr	Ala	Lys	Leu	Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp	
		35					40					45				
gtc	caa	gat	gaa	tta	ggt	cac	tca	gtt	gtc	gag	gcc	atc	ggc	act	tcc	192
Val	Gln	Asp	Glu	Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser	
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aat	tcc	atc	tac	atc	cac	tgc	gat	gtt	acc	aat	gaa	gac	gat	gtt	aaa	240
Asn	Ser	Ile	Tyr	Ile	His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Asp	Val	Lys	
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aat	gcc	gtg	gac	aac	aca	gtt	tca	acc	tat	gga	aaa	ctg	gac	att	atg	288
Asn	Ala	Val	Asp	Asn	Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met	
			85					90						95		
ttc	aac	aat	gca	gga	att	gct	gac	ccc	aac	aag	ccc	cgc	atc	gta	gac	336
Phe	Asn	Asn	Ala	Gly	Ile	Ala	Asp	Pro	Asn	Lys	Pro	Arg	Ile	Val	Asp	
			100					105					110			
aac	gaa	aaa	gca	gac	ttt	gaa	cgc	gtt	ctc	agc	gta	aat	gta	acc	ggt	384
Asn	Glu	Lys	Ala	Asp	Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly	
		115					120					125				
gtt	ttc	cta	tgc	atg	aag	cac	gca	gca	cgc	gtt	atg	gtg	cca	gca	cgc	432
Val	Phe	Leu	Cys	Met	Lys	His	Ala	Ala	Arg	Val	Met	Val	Pro	Ala	Arg	
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agt	ggc	agc	ata	att	tcc	act	gct	agc	gta	agc	tca	aca	att	ggt	ggt	480
Ser	Gly	Ser	Ile	Ile	Ser	Thr	Ala	Ser	Val	Ser	Ser	Thr	Ile	Gly	Gly	
	145				150				155					160		
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Ala	Ala	Ser	His	Ala	Tyr	Cys	Cys	Ser	Lys	His	Ala	Val	Leu	Gly	Leu	
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act	agg	aat	ctg	gca	gtc	gag	ctc	gga	caa	ttt	ggc	att	agg	gtt	aat	576
Thr	Arg	Asn	Leu	Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn	
			180					185					190			
tgt	ttg	gct	cct	tac	gcg	ctt	gct	acg	cct	tta	gcc	aag	aaa	ttt	gta	624
Cys	Leu	Ala	Pro	Tyr	Ala	Leu	Ala	Thr	Pro	Leu	Ala	Lys	Lys	Phe	Val	
		195					200					205				
ggg	ctt	gaa	aat	gac	gaa	gat	ttg	gag	aat	gca	atg	agc	ctt	atg	gga	672
Gly	Leu	Glu	Asn	Asp	Glu	Asp	Leu	Glu	Asn	Ala	Met	Ser	Leu	Met	Gly	

210	215	220	
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct			720
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala			
225	230	235	240
ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg			768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
	245	250	255
ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc			816
Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe			
	260	265	270
caa tat cca gac act			831
Gln Tyr Pro Asp Thr			
	275		

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 <213> Forsythia x intermedia

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 35 40 45
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
 50 55 60
 Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys
 65 70 75 80
 Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
 85 90 95
 Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp
 100 105 110
 Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly
 115 120 125
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg
 130 135 140
 Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly

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	180	185	190			
Cys Leu Ala Pro	Tyr Ala Leu Ala	Thr Pro Leu Ala	Lys Lys Phe Val			
	195	200	205			
Gly Leu Glu Asn	Asp Glu Asp Leu	Glu Asn Ala Met	Ser Leu Met Gly			
	210	215	220			
Asn Leu Lys Gly	Thr Asn Leu Lys	Ala Glu Asp Val	Ala Asn Ala Ala			
	225	230	235	240		
Leu Tyr Leu Ala	Ser Asp Glu Ala	Lys Tyr Val Ser	Gly His Asn Leu			
	245	250	255			
Phe Ile Asp Gly	Gly Phe Ser Val	Tyr Asn Ser Ala	Ile Lys Met Phe			
	260	265	270			
Gln Tyr Pro Asp	Thr					
	275					

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1 5 10 15	
aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca	96
Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr	
20 25 30	
gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc	144
Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val	
35 40 45	
caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat	192
Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn	
50 55 60	

tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat	240
Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn	
65 70 75 80	
gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc	288
Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe	
85 90 95	
aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac	336
Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn	
100 105 110	
gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt	384
Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val	
115 120 125	
ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt	432
Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser	
130 135 140	
ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt	480
Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly	
145 150 155 160	
tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act	528
Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr	
165 170 175	
agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt	576
Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys	
180 185 190	
ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg	624
Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly	
195 200 205	
att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat	672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn	
210 215 220	
ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt	720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu	
225 230 235 240	
ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc	768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe	
245 250 255	
atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa	816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln	
260 265 270	
tat cca gac tct	828

Tyr Pro Asp Ser
275

<210> 10

<211> 276

<212> PRT

<213> Forsythia x intermedia

<400> 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
1 5 10 15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
20 25 30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
35 40 45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
50 55 60

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
65 70 75 80

Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
85 90 95

Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
100 105 110

Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
115 120 125

Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
130 135 140

Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
145 150 155 160

Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
165 170 175

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
180 185 190

Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
195 200 205

Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
210 215 220

Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu

225 230 235 240
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
 245 250 255
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
 260 265 270
Tyr Pro Asp Ser
 275

<210> 11
<211> 21
<212> PRT
<213> Forsythia x intermedia

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> N-terminal peptide of F. intermedia
 secoisolariciresinol protein wherein Xaa at
 positions 3, 12 and 20 represents an unidentified
 amino acid residue

<400> 11
Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
 1 5 10 15

Ile Thr Gly Xaa Ala
 20

<210> 12
<211> 17
<212> PRT
<213> Forsythia x intermedia

<400> 12
Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
 1 5 10 15

Lys

<210> 13
<211> 15
<212> PRT
<213> Forsythia x intermedia

<400> 13
Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys

1. 5 10 15

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3, 9, 15 and 18
represents inosine

<400> 14
ggnathggng aracnacngc 20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 15
ccngcrttng araacatdat 20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)

<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 16

ccngcrttnc traacatdat

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer

<400> 17

attccgctag attgcattga

20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3 and 9
represent inosine

<400> 18

ccngcrttnc traacatdat

20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaccct cactaaaggg

20

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer

<400> 20
cagcttcgaa ctgcattcgc aag

23

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(22)
<223> T7 PCR primer

<400> 21
cgggatatca ctcagcataa tg

22

<210> 22
<211> 816
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(816)

<400> 22

cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt	48
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu	
1 5 10 15	
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc	96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe	
20 25 30	
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta	144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu	
35 40 45	
ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc	192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile	
50 55 60	
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac	240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn	
65 70 75 80	
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga	288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly	
85 90 95	
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac	336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp	
100 105 110	
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg	384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met	
115 120 125	
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att	432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile	
130 135 140	
tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat gcc	480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala	
145 150 155 160	
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca	528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala	
165 170 175	
gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc	576
Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe	
180 185 190	
ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa	624
Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu	
195 200 205	

gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca 672
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
 210 215 220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt 720
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
 225 230 235 240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg 768
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
 245 250 255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct 816
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
 260 265 270

<210> 23

<211> 272

<212> PRT

<213> Forsythia x intermedia

<400> 23

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
 1 5 10 15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
 20 25 30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
 35 40 45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
 50 55 60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
 65 70 75 80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
 85 90 95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
 100 105 110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
 115 120 125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
 130 135 140

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
 145 150 155 160

Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
165 170 175
Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
180 185 190
Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
195 200 205
Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
210 215 220
Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
225 230 235 240
Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
245 250 255
Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
260 265 270

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 24
acatatgcag cttcgaactg cattcgcaag aag

33

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)

<223> PCR primer

<400> 25

catatgggca gacatggtac atgatcaatt gca

33